

# Brain Tumor Detection and Classification

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**Abstract—** Brain is the most crucial organ in our body. Unfortunately, due to abnormal growth of the cell in the brain, it may cause tumors. Tumors may be benign and malignant. Regardless, it is important for an early detection to be done in order to give the right treatment. The focus of this study is to formulate the best method to preprocess MRI images of a brain, extract its features, and use it to make predictions about whether a patient has a tumor and what kind using machine learning. There are 2 ways that are compared to segment the tumor: U-Net pretrained model and Thresholding. The results shows that models that are trained using images segmented by U-Net performs significantly better than thresholding. However, the best performing model with U-Net is Logistic Regression, while Random Forest performs the best with thresholding.

**Keywords—** Brain tumor, MRI, machine learning, feature extraction, SVM, thresholding, image classification

## I. INTRODUCTION

The brain controls everything, from moving and thinking to breathing and heartbeats. It helps different organs work together and allows us to make decisions. It also processes information and responds to changes inside and outside the body [23].

Brain tumors, an abnormal cluster of cells that

grow within human brain tissue, can be classified into benign (non-cancerous) and malignant (cancerous) tumors. Cells in benign tumors generally grow slowly, lack invasiveness and metastasis, and can be surgically removed without significantly affecting the patients' survival rate. While the survival rate varies significantly between benign and malignant brain tumors, the complexity of brain tumor diagnosis is further compounded by the diverse anatomical locations where these abnormal growths can develop [24]. Brain tumors can emerge in critical regions such as the cerebrum, cerebellum, brainstem, and other intricate neural areas, making their detection and precise localization extremely challenging for medical professionals.

Given these challenges, advanced imaging techniques are essential for early detection and accurate diagnosis of brain tumors. Magnetic Resonance Imaging (MRI) has become a primary imaging modality for brain tumor detection due to its ability to provide high-resolution, multi-modal images that enhance diagnostic accuracy.

## II. LITERATURE REVIEW

The research shows that the edges of the tumor are sometimes not detected, and if not preserved, those edges could be lost [14][15]. So in this project, all MR images are passed through the Wiener filter for noise suppression and edge preservation.

In order to perform histogram equalization in localized areas for contrast improvement and to

ensure that the tumor region is visible despite the image having surrounding brighter and darker places, Contrast Limited Adaptive Histogram Equalization (CLAHE) is utilized [16][17].

Normalization for pixel intensity is crucial. All images must be at a level of brightness and contrast, equalized among the input files without disturbing model interpretation and error analysis of output. Moreover, normalization via histograms is explored to avoid a gradual increase or decrease in intensity because of separately scanned results [18][19][20]. In addition, images are brightness adjusted and horizontally flipped at random to avoid overfitting and allow for generalizations [21][19].

Segmentation is necessary to determine the exact boundaries of aberrant growth in order to distinguish tumors from brain tissue in MRI images. Two different segmentation techniques are used and compared in this study: Thresholding, a conventional intensity-based technique that divides areas according to the intensity of pixels, and U-Net is a deep learning architecture created especially for biomedical image segmentation. It can precisely define tumor boundaries by capturing both local and global context.

There have been studies conducted for brain tumor detection that utilize Local Binary Pattern (LBP) as one of the features [22][23]. In essence, LBP is a local texture representation of an image that works by taking a pixel, and then comparing it with all of its neighbors. This will be useful when detecting tumors because cancer (and by extension a tumor) shows uncontrolled cellular growth, which changes the cell arrangement of the tissues [24]. This change in the texture of the tissue can be captured by LBP. However, it is important to note that the LBP image itself is not what will be used as features, but rather the histogram of the LBP image [25].

In order to better detect patterns that are indicative of a tumor, the Gabor Wavelet Transform (GWT) will be implemented using the Gabor filter. For this specific case, tumors have irregular textural patterns that differentiate them from other healthy tissues. These slight variations are sometimes hard to detect with regular image processing techniques. With GWT, a more thorough extraction of features can be done to better detect the irregularities, or the

tumors, in the image [26]. Study shows that GWT does help in tumor segmentation, due to GWT's ability to decompose images into frequencies and orientations [27][28].

The Gray-Level Co-occurrence Matrix (GLCM) is a statistical method used for texture analysis by examining the spatial relationships between pixel intensities in an image. GLCM extracts crucial textural features such as contrast, correlation, energy, and homogeneity by computing the frequency of pixel pairs at specific distances and orientations. These features help characterize the surface properties of an image, making GLCM an effective tool for analyzing complex patterns and structures [29]. In the context of brain tumor segmentation and classification, GLCM plays a vital role in feature extraction, enabling machine learning models to differentiate between healthy and abnormal tissues. Since tumors often exhibit distinct textural properties compared to normal brain tissue, GLCM-derived features enhance classification accuracy by providing detailed information about image textures.

In classification, SVM has been known for its strong results on medical image classification, particularly when working with high-dimensional and structured feature sets. It is a supervised learning algorithm that aims to find the optimal hyperplane [30] that best separates data points of different classes—in this case, MRI images with and without tumors.

### III. METHODOLOGY

#### A. Enhancement

This phase aims to achieve the highest possible image quality using a two-stage method. Noise reduction is achieved using a Wiener filter on the data, which removes Gaussian noise and keeps important information about the tumor's border [6]. Because this adaptive filter effectively minimizes the error when removing noise, it is especially suitable for MRI images, where the important details of the anatomy must be kept[9].

Once denoising happens, Contrast-Limited Adaptive Histogram Equalization (CLAHE) enhances local contrast by splitting the image into small areas (tiles) and using histogram equalization with a clip limit 2.0. Thanks to this technique, small

areas throughout tissues are not artificially increased, but regions with tumors can be shown more clearly (*Iraqi Journal of Science*, 2024). Many people praise CLAHE for highlighting different textures and intensity variations in brain tumors, making it possible to spot low-contrast tumors more easily[9].

Wiener filtering and CLAHE are used in MRI to solve the problems of interference from noise and the low contrast the scans usually display. Studies show that boosting EnhanceNet Colour by EnhanceNet helps clear up images and boosts the quality of tasks like segmentation and classification [6][9].

#### B. Normalization

Applying normalization to brain MRIs before analysis is important to handle variations in imaging intensity caused by equipment, different procedures, or individual factors in patients. This method involves splitting every pixel value by 255.0, which helps to scale back the 8-bit image intensities [0, the original range]. It fixes the scaling level at 255 because of the 8-bit standard, so the same scaled values can be used for every image.

Almost all deep learning applications in medical image processing rely on normalization because different data sets are handled the same, and training is more effective. When the pixel values are scaled, all image data is treated the same way, reducing optimization risks and allowing further enhancement, augmentation, and segmentation steps to work well with similar data sets [7][8]. In addition, normalizing the data makes it possible to repeat and strengthen the results of extraction and classification after segmentation.

#### C. Cropping

MRI images undergo automated cropping to standardize input sizes and focus computational resources on the brain region. The process begins with grayscale conversion followed by Gaussian blurring ( $3 \times 3$  kernel) to reduce noise. A binary mask is generated using thresholding (45/255), isolating the brain from the background. Morphological operations (2 iterations of erosion followed by dilation) refine the mask by removing

minor artifacts. The largest contour in the mask is identified, and its bounding box coordinates are extracted. An optional margin parameter expands the bounding box to preserve peripheral brain tissue. The original image and corresponding mask are cropped to these coordinates if available, ensuring consistent input dimensions for subsequent processing stages. This spatial standardization improves the reliability of enhancement, normalization, and segmentation steps by eliminating irrelevant background variability.

#### D. Augmentation

Taking steps to increase our datasets with similar images is very useful for medical imaging, particularly when working with brain MRI, since the quantity of labeled data is often low and some classes are very few. This method's training data is modified to make it more diverse, which should help the segmentation model work better in different cases. Most augmentation techniques applied are horizontal flipping and adjusting the image's brightness. Random horizontal flipping exploits the almost identical right and left hemispheres in axial brain MRIs, which introduces changes across slices and assists the model in focusing on important but consistent features. Instead, by adjusting brightness, the software tries to simulate how the scanner would adjust, and the patient's unique factors might affect the image's overall intensity. Therefore, the model feels less threatened by changes in the quality of the input images and can be applied more successfully in various study situations.

Most modern brain tumor segmentation models use these augmentation approaches, which recent research has shown to improve the results of deep learning tools in medical imagery. Using these techniques allows the methodology to fit the high standards in the field and leads to models that better handle the natural variability present in real-world clinical MRI images[9].

#### E. Segmentation

The segmentation methodology includes two different but complementary techniques: hybrid entropy-MultiOtsu thresholding and the 2D U-Net,

which is based on deep learning. Each technique is intended to resolve distinct issues in the analysis of brain tumor MRI scans, ensuring strong performance for various types of tumors.

The approach hybrids the idea of analyzing texture and setting a threshold level based on intensity to find tumors. Scientists use local entropy with a 5-pixel disk kernel to determine textural details, which helps them isolate the parts of tumor tissue with firm heterogeneity [10]. Entropy below 0.5625 is set as black, and higher entropy values are set as white. In addition, MultiOtsu thresholding separates the MRI into three parts, marking the area with the highest intensity since it is most likely to contain the tumor [11]. Pixels are kept only if they satisfy both conditions when the bits are compared with bitwise AND. The mask is improved by applying a 5-pixel elliptical kernel, which cleans up noise and makes edges smoother [10][11]. It is most effective for fast computing and easy understanding when assessing high-contrast tumors.

At the same time, the 2D U-Net model is built using an encoder-decoder structure and skip connections to find the position of tumors precisely [12]. The model is trained with external data marked by humans and mixes Dice and binary cross-entropy loss functions to deal with the uneven number of classes and outputs maps with probability values for every pixel. Maps are processed using a threshold of 0.5 to get masks with only two values: 0 or 1. Methods such as flipping images and adjusting brightness make the model more resistant to variations in MRI data, and the best checkpoint is chosen by examining validation Dice scores [13][12]. U-Net does well in complex cases such as diffuse or low-contrast tumors because it relies on learned features from a wide range of data.

Whereas hybrid thresholding is helpful for quickly precisely highlighting well-defined tumors, U-Net works well when adapting to heterogeneous lesions. Features are determined from the outputs of each segmentation, which helps display the tumor's characteristics needed for classification. Using this two-method system helps us analyze things from multiple angles, honoring interpretability as well as fast and effective working [10][11][12] [13].

#### F. Local Binary Pattern (LBP)

Local Binary Patterns (LBP) [2] is a simple yet effective texture descriptor that compares each pixel to its circular neighborhood. In our implementation, each grayscale pixel in the segmented tumor region is compared with its  $P=8$  neighbors on a circle of radius  $R=1$  using the “uniform” pattern method. Specifically, for every center pixel, each neighbor is assigned a 1 if its intensity is greater than or equal to the center or a 0 otherwise, these eight binary values form a uniform LBP code. We then compute a histogram of these codes using  $P+2=10$  bins (to capture all uniform patterns plus one bin for nonuniform patterns). Finally, we normalize the histogram via  $L1$  normalization so that the sum of its entries is 1. This 10-dimensional feature vector succinctly captures local texture variations across the tumor ROI and was found to improve classification accuracy compared to a non-uniform 256-bin approach.

#### G. Gabor Wavelet Transform (GWT)

Gabor filters capture multiscale and orientation-specific texture information, which is valuable for distinguishing tumor boundaries [3]. We first convert each segmented tumor image to grayscale and then apply a bank of Gabor filters at two spatial frequencies,  $f \in \{0.1, 0.3\}$ , and at four orientations,  $\theta \in \{0, \pi/4, \pi/2, 3\pi/4\}$ . For each  $(f, \theta)$  pair, we use the real component of the Gabor response returned by `skimage.feature.gabor`. From that real response, we compute its mean and its variance. Concatenating these statistics over all  $2 \times 4 = 8$  filter configurations yields a 16-dimensional GWT feature vector. These mean and variance values summarize how strongly each frequency-orientation pattern is present in the tumor region, helping to capture both coarse and fine directional textures.

#### H. Gray Level Co-Occurrence Matrix (GLCM)

GLCM features quantify how often pairs of gray levels occur at a specified offset, capturing second-order texture patterns [4]. In our implementation, the tumor region of interest is converted to an 8-bit grayscale image with intensity values ranging from 0 to 255. We then compute the

GLCMs using a pixel distance of 1 and four angles: 0,  $\pi/4$ ,  $\pi/2$ , and  $3\pi/4$ . Each GLCM is normalized and made symmetric. From each directional matrix, we extract six Haralick properties: contrast, dissimilarity, homogeneity, angular second moment (ASM), energy, and correlation, using the greycoprops function. Because we consider four directions, each property yields four values, resulting in a total of 24 features. Although averaging across directions is a common approach, we found that preserving all directional values provided better classification performance by retaining orientation-sensitive texture details.

### I. Machine Learning Classification

In this project, we focused on traditional machine learning methods to classify brain MRI images as either containing a tumor or not. Although we initially considered several modeling approaches—including deep learning and hybrid methods, we ultimately chose to work entirely with classical machine learning techniques due to the scope and limitations of the project. Support Vector Machine (SVM) was chosen as our primary model, as it was part of the original proposal and is widely known for its effectiveness in medical image classification [5].

Besides SVM, we also experimented with other popular machine learning models to compare their performance using the same extracted features. These models include Logistic Regression, Random Forest, and Gradient Boosting. To improve overall classification results, we also used a Voting Ensemble method. This ensemble combines predictions from all the individual classifiers and uses a majority vote system to make the final decision.

To evaluate and compare model performance, we used the following standard classification metrics:

- **Accuracy:** Measures the proportion of correctly classified images.
- **Precision:** Indicates the proportion of positive identifications (tumors) that were actually correct.
- **Recall (Sensitivity):** Measures how well the model detects actual tumor cases.

- **F1-Score:** The harmonic mean of precision and recall, especially useful in imbalanced datasets.

These metrics were computed for each model using both **thresholding** and **U-Net** segmentation outputs. F1-score was given particular attention due to its balance between false positives and false negatives, which is important in medical diagnosis.

==== SVM ===					
	precision	recall	f1-score	support	
0	0.95	0.94	0.94	298	
1	0.91	0.85	0.88	269	
2	0.85	0.90	0.87	256	
3	0.89	0.91	0.90	320	
accuracy			0.90	1143	
macro avg	0.90	0.90	0.90	1143	
weighted avg	0.90	0.90	0.90	1143	

### IV. RESULTS AND DISCUSSIONS

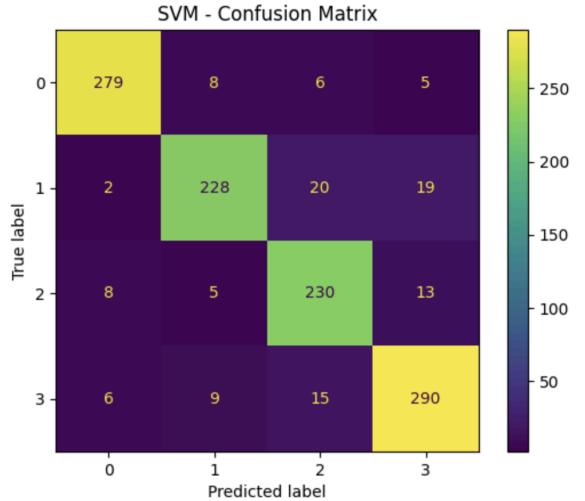


Fig.1 Classification score and confusion matrix of the SVM model using U-Net segmentation.

Using the SVM model along with the proposed method, it yielded an accurate result. Recall that for segmentation, there were 2 methods proposed: U-Net segmentation and thresholding. Using U-Net

segmentation, the SVM model scored a weighted F1-score of 90% (Fig.1), while the thresholding method falls short at 84% weighted average F1 score (Fig. 2). In the medical world, it is also worth noting that the weighted recall for both U-Net and thresholding segmentation is also 90% and 84% respectively, which indicates

that the risk of false negatives is low.

```
==== SVM ====
Accuracy: 0.8381452318460193
F1 Score: 0.8376858187728878
      precision    recall  f1-score   support
0       0.93     0.94    0.94      298
1       0.81     0.75    0.78      269
2       0.73     0.75    0.74      256
3       0.87     0.88    0.88      320
accuracy                           0.84      1143
macro avg       0.83     0.83    0.83      1143
weighted avg    0.84     0.84    0.84      1143
```

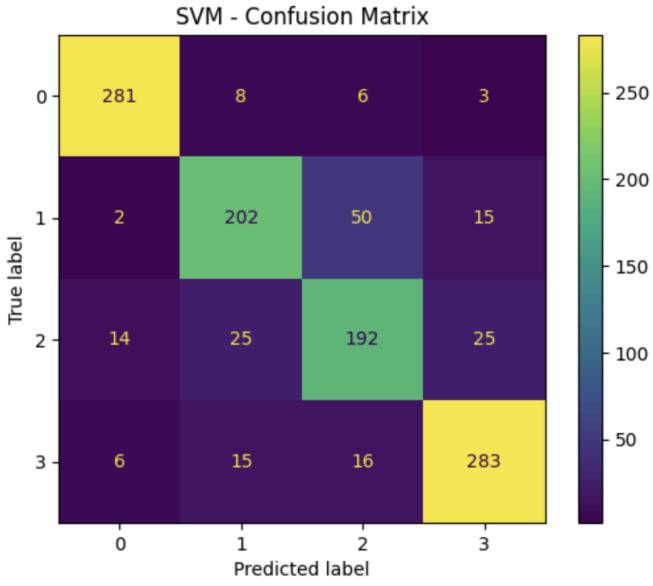


Fig. 2 Classification score and confusion matrix of the SVM model using thresholding segmentation.

One visual proof that could explain why U-Net performs better is the segmentation result. For U-Net, since it is a pretrained segmentation model, it produces a more focused segmentation around the tumor. As for thresholding, the segmentation is not always consistent. From Fig. 3, it can be observed that the segmented section is not only the tumor, but also around the skull itself.

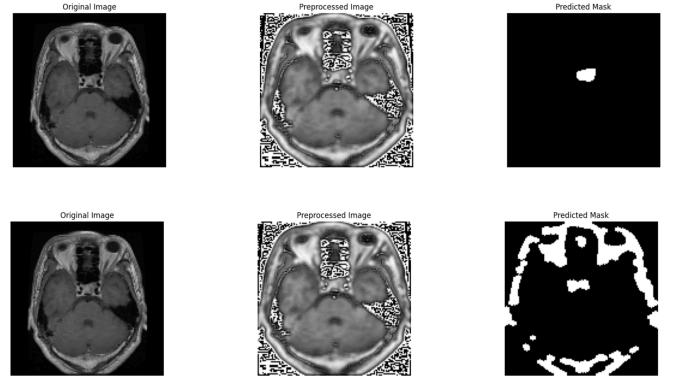


Fig. 3 A comparison of segmentation quality using U-Net (top) and using thresholding (bottom).

## V. COMPARISONS

The experiment was run on multiple models, which are logistic regression, random forest, gradient boost, and combine those models with a voting ensemble. There were also 2 proposed segmentation methods: U-Net segmentation and thresholding. It turns out logistic regression model performs the best (Tab. 1) because it is simple, efficient, and well-suited to linearly separable data. The extracted features from LBP, GLCM, and Gabor filters may have provided sufficient information for logistic regression to make accurate predictions without the need for more complex models.

Model	U-Net (F-1 Score)
Logistic regression	92.05%

Random forest	90%
Gradient boost	89%
Voting ensemble	92.03%

Tab. 1 F1-scores of each classification model using U-Net segmentation.

While using thresholding, it turns out the random forest model performs the best (Tab. 2) because it is able to handle non-linear patterns and noisy features more effectively. Random Forest builds multiple decision trees and combines their results, which helps improve stability and accuracy.

Model	Thresholding (F-1 Score)
Logistic regression	84%
Random forest	86.23%
Gradient boost	84%
Voting ensemble	85.79%

Tab. 2 F1-scores of each classification model using thresholding segmentation.

## VI. CONCLUSIONS

This work presented a traditional machine learning pipeline for brain tumor classification, developed under the constraint of excluding deep learning methods. We focused on leveraging handcrafted features including Local Binary Patterns (LBP), Gabor Wavelet Transform (GWT), and Gray-Level Co-occurrence Matrix (GLCM) to capture key texture characteristics of brain MRI scans. These features were then used to train and evaluate several conventional classifiers, including Support Vector Machines and Logistic Regression.

Our results show that this pattern recognition-based approach can deliver strong performance, particularly when combined with accurate segmentation such as that produced by a pretrained U-Net model. The best-performing configuration, which used U-Net segmentation and logistic regression, achieved an F1-score exceeding

92 percent. While deep learning remains the dominant approach in modern medical image analysis, this study demonstrates the continued value of classical methods in contexts where model simplicity, interpretability, or data limitations are important.

Future work may extend this pipeline toward multiclass tumor subtype classification or explore hybrid approaches that combine handcrafted and learned features to enhance performance further.

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